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## SEARCH REQUEST FORM

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### Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

### STAFF USE ONLY

Date completed: 08-15-02

Searcher: Beverly CASS

Terminal time: 2:22

Elapsed time: 4:45

CPU time: 3:55

Total time: 3:55

Number of Searches: 1

Number of Databases: 2

#### Search Site

STIC

CM-1

Pre-S

#### Type of Search

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

#### Vendors

IG

STIN

Dialog

APS

Geminfo

SDC

DARC/Qwestel

Other

CGN

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Parkin  
09/605573

09/605573

FILE 'REGISTRY' ENTERED AT 15:39:41 ON 15 AUG 2002  
L1 1 S GRETLMQDQQRLNSWGCKGRIICYTSARWH/SQSP

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2002 ACS  
RN 275801-53-1 REGISTRY  
CN 135: PN: JP2000157268 SEQID: 69 unclaimed sequence (9CI) (CA INDEX  
NAME)  
SQL 30

SEQ 1 GRETLMQDQQ RLNSWGCKGR IICYTSARWH  
===== ===== =====  
HITS AT: 1-30

REFERENCE 1: 133:55969

FILE 'HCAPLUS' ENTERED AT 15:40:58 ON 15 AUG 2002  
L2 1 S L1

L2 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2002 ACS  
ACCESSION NUMBER: 2000:392837 HCAPLUS  
DOCUMENT NUMBER: 133:55969  
TITLE: Peptide for detection of Group O HIV-1 and use  
for diagnosis  
INVENTOR(S): Deleys, Robert; Chen, Jan  
PATENT ASSIGNEE(S): Ortho-Clinical Diagnostics, Inc., USA  
SOURCE: Jpn. Kokai Tokkyo Koho, 103 pp.  
CODEN: JKXXAF  
DOCUMENT TYPE: Patent  
LANGUAGE: Japanese  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2000157268	A2	20000613	JP 1999-338385	19991129
US 6149910	A	20001121	US 1999-433428	19991104
EP 1013766	A2	20000628	EP 1999-309491	19991129

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,  
PT, IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.: US 1998-110292P P 19981130  
US 1999-119138P P 19990208  
US 1999-433428 A 19991104

AB Disclosed are the peptides derived from the immunodominant region of  
the Group O HIV-1 gp41 envelope protein, which do not correspond to  
any known naturally occurring Group O sequence or variant. The  
peptides bind to the antibodies to Group O HIV-1. The peptides are  
useful in detecting antibodies arise from the infection by Group O  
HIV-1. The peptides may be prepd. in a hybrid form with that of  
Group M HIV-1.

IT 275801-53-1  
RL: PRP (Properties)  
(unclaimed sequence; peptide for detection of Group O HIV-1 and  
use for diagnosis)

FILE 'HOME' ENTERED AT 15:41:07 ON 15 AUG 2002

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OM protein - protein search, using sw model

Run on:

August 15, 2002, 10:11:26 ; Search time 30.17 seconds

(without alignments)

110.448 Million cell updates/sec

Title:

US-09-605-573a-69

Perfect score:

173 GRETLMQDQRNLNSWGCKGRITCYTSARWH 30

Sequence:

BLOSUM62

Scoring table:

Gapop 10.0 , gapext 0.5

Searched:

747574 seqs, 111073796 residues

Post-processing:

Minimum Match 0%

Maximum Match 100%

Number of hits satisfying chosen parameters:

747574

Database :

A\_Geneeseq\_032802.\*

1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*

2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*

3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:\*

4: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:\*

5: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:\*

6: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:\*

7: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:\*

8: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:\*

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11: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:\*

12: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:\*

13: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:\*

14: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:\*

15: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:\*

16: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:\*

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19: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:\*

20: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:\*

21: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:\*

22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Query	Match Length	DB ID	Description
1	173	100.0	30	21	AAB12264	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.
2	157	90.8	35	21	AAB12259	HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection; acquired immunodeficiency syndrome; group O HIV; gp41.
3	157	90.8	149	21	AAB12262	KW
4	157	90.8	220	22	AAB12261	KW
5	157	90.8	368	21	AAB12253	KW
6	90.8	439	21		AAB12252	OS
7	89.6	28	155	21	AAB12257	XX
8	134	77.5	23	21	AAB12256	XX
9	76.9	23	133	21	AAB12254	XX
10	76.3	23	132	21	AAB12255	PT
11	75.7	33	21		AAB12236	PT

Result	No.	Score	Query	Match Length	DB ID	Description
1	173	100.0	30	21	AAB12264	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.
2	157	90.8	35	21	AAB12259	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.
3	157	90.8	149	21	AAB12262	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.
4	157	90.8	220	22	AAB12261	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.
5	157	90.8	368	21	AAB12253	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.
6	90.8	439	21		AAB12252	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.
7	89.6	28	155	21	AAB12257	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.
8	134	77.5	23	21	AAB12256	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.
9	76.9	23	133	21	AAB12254	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.
10	76.3	23	132	21	AAB12255	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.
11	75.7	33	21		AAB12236	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.

#### ALIGNMENTS

RESULT	1					
ID	AAB12264					
	AAB12264 standard; peptide: 30 AA					
XX						
AC	AAB12264;					
XX						
DT	10-NOV-2000 (first entry)					
DE	HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.					
XX						
KW	HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection; acquired immunodeficiency syndrome; group O HIV; gp41.					
XX						
OS	Human immunodeficiency virus type 1.					
XX						
PN	EP1013766-A2.					
XX						
PD	28-JUN-2000.					
XX						
PF	29-NOV-1999; 99EP-0309491.					
PR	30-NOV-1998; 98US-0110292.					
PR	08-FEB-1999; 99US-0119138.					
PR	04-NOV-1999; 99US-0433428.					
PA	(ORFH-) ORTHO-CLINICAL DIAGNOSTICS INC.					
XX						
PT	De Ley R, Zheng J;					
PT	De Ley R, Zheng J;					
XX						
DR	WPI; 2000-402205/35.					
PT	New antigenic peptides and peptide functional derivatives, useful for detection of antibodies produced in response to human immunodeficiency virus group O antibodies.					



**RESULT** 4  
 OS Human immunodeficiency virus type 1.  
 OS Unidentified.  
 OS AAB12261 standard; peptide; 220 AA.  
 XX  
 ID AAB12261  
 XX  
 AC  
 XX  
 DT 10-NOV-2000 (first entry)  
 XX  
 DE HIV group M/ group O mosaic protein # 1.  
 XX  
 PR HIV-1; AIDS; human immunodeficiency virus type 1;  
 KW acquired immunodeficiency syndrome; group O HIV; gp41.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN EP1013766-A2.  
 XX  
 PR 28-JUN-2000.  
 XX  
 PR 29-NOV-1999; 99EP-0309491.  
 XX  
 PR 30-NOV-1998; 98US-0110292.  
 XX  
 PR 08-FEB-1999; 99US-0119138.  
 XX  
 PR 04-NOV-1999; 99US-0433428.  
 XX  
 PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.  
 XX  
 PI De Leys R, Zheng J;  
 XX  
 DR WPI; 2000-402205/35.  
 XX  
 PR 29-NOV-1999; 99EP-0309491.  
 XX  
 PR 30-NOV-1998; 98US-0110292.  
 XX  
 PR 08-FEB-1999; 99US-0119138.  
 XX  
 PR 04-NOV-1999; 99US-0433428.  
 XX  
 PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.  
 XX  
 PI De Leys R, Zheng J;  
 XX  
 DR WPI; 2000-402205/35.  
 XX  
 PR New antigenic peptides and peptide functional derivatives, useful for  
 PT detection of antibodies produced in response to human immunodeficiency  
 PR virus group O antibodies -  
 XX  
 PS Claim 15; Page 37-38; 52pp; English.  
 CC Human Immunodeficiency Virus (HTV) is the principle aetiological  
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV  
 CC envelope protein, and may be used as an antigen for the detection of  
 CC antibodies produced in response to HIV infection. Mosaic gp41 proteins  
 CC were constructed, in which the immunodominant region of group M HIV was  
 CC replaced by the corresponding region from group O HIV. The mosaic gp41  
 CC proteins would be useful as antigens, used in the detection of anti-group  
 CC HIV antibodies produced in response to HIV infection. The present  
 CC sequence is a dihydrofolate reductase (DHFR) fusion protein of one such  
 CC mosaic protein.  
 XX  
 SQ Sequence 368 AA:  
 CC Human Immunodeficiency Virus (HTV) is the principle aetiological  
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV  
 CC envelope protein, and may be used as an antigen for the detection of  
 CC antibodies produced in response to HIV infection. Mosaic gp41 proteins  
 CC were constructed, in which the immunodominant region of group M HIV was  
 CC replaced by the corresponding region from group O HIV. The mosaic gp41  
 CC proteins would be useful as antigens, used in the detection of anti-group  
 CC HIV antibodies produced in response to HIV infection. The present  
 CC sequence is one such mosaic protein.  
 XX  
 O Sequence 220 AA:  
 CC Human Immunodeficiency Virus (HTV) is the principle aetiological  
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV  
 CC envelope protein, and may be used as an antigen for the detection of  
 CC antibodies produced in response to HIV infection. Mosaic gp41 proteins  
 CC were constructed, in which the immunodominant region of group M HIV was  
 CC replaced by the corresponding region from group O HIV. The mosaic gp41  
 CC proteins would be useful as antigens, used in the detection of anti-group  
 CC HIV antibodies produced in response to HIV infection. The present  
 CC sequence is one such mosaic protein.  
 XX  
 RESULT 5  
 Query Match 90.8%; Score 157; DB 21; Length 220;  
 Best Local Similarity 96.4%; Pred. No. 1.e-14;  
 Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 ETLMQDQORLNNSWCKGKICLYSARWH 30  
 Db 44 etlmnqndqrlnswckgrlicytsarwh 71  
 XX  
 O Sequence 368 AA:  
 CC Human Immunodeficiency Virus (HTV) is the principle aetiological  
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV  
 CC envelope protein, and may be used as an antigen for the detection of  
 CC antibodies produced in response to HIV infection. Mosaic gp41 proteins  
 CC were constructed, in which the immunodominant region of group M HIV was  
 CC replaced by the corresponding region from group O HIV. The mosaic gp41  
 CC proteins would be useful as antigens, used in the detection of anti-group  
 CC HIV antibodies produced in response to HIV infection. The present  
 CC sequence is one such mosaic protein.  
 XX  
 RESULT 6  
 AAB12252  
 ID AAB12252 standard; peptide; 439 AA.  
 XX  
 AC AAB12252;  
 XX  
 DT 10-NOV-2000 (first entry)  
 XX  
 DE DHFR-hENV-MH fusion protein.  
 XX  
 PR HIV-1; AIDS; human immunodeficiency virus type 1; DHFR-hENV-MH;  
 KW acquired immunodeficiency syndrome; group O HIV; gp41.  
 XX  
 OS Human immunodeficiency virus type 1.  
 OS Unidentified.  
 XX  
 PN EP1013766-A2.  
 XX  
 PD 28-JUN-2000.  
 XX  
 PR 29-NOV-1999; 99EP-0309491.  
 XX  
 PR 30-NOV-1998; 98US-0110292.  
 XX  
 PR 08-FEB-1999; 99US-0119138.  
 XX  
 PR 04-NOV-1999; 99US-0433428.  
 XX  
 PR DHFR-hES-MH fusion protein.  
 XX  
 PR HIV-1; AIDS; human immunodeficiency virus type 1; DHFR-hES-MH;  
 KW acquired immunodeficiency syndrome; group O HIV; gp41.  
 XX  
 OS Human immunodeficiency virus type 1.  
 OS Unidentified.  
 XX  
 PN EP1013766-A2.  
 XX  
 PD 28-JUN-2000.  
 XX  
 PR 29-NOV-1999; 99EP-0309491.  
 XX  
 PR 30-NOV-1998; 98US-0110292.  
 XX  
 PR 08-FEB-1999; 99US-0119138.  
 XX  
 PR 04-NOV-1999; 99US-0433428.  
 XX

XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.  
 PA PT virus group O antibodies -  
 XX XX  
 PI PS Claim 1; Page 36; 52pp; English.  
 XX  
 DR WPI; 2000-402205/35.  
 XX New antigenic peptides and peptide functional derivatives, useful for  
 PT detection of antibodies produced in response to human immunodeficiency  
 virus group O antibodies -  
 XX  
 PS Example 5; FIG 6; 52pp; English.  
 CC Human Immunodeficiency Virus (HIV) is the principle aetiological  
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV  
 envelope protein, and may be used as an antigen for the detection of  
 CC antibodies produced in response to HIV infection. Mosaic gp41 proteins  
 CC were constructed, in which the immunodominant region of group M HIV was  
 CC replaced by the corresponding region from group O HIV. The mosaic gp41  
 CC proteins would be useful as antigens, used in the detection of anti-group  
 O HIV antibodies produced in response to HIV infection. The present sequence  
 CC is a dhydrofolate reductase (DHFR) fusion protein of one such  
 CC mosaic protein.  
 XX  
 Sequence 439 AA;

Query	Match	Score	Length
Best Local Similarity	90.8%	157	DB 21;
Matches	96.4%	Pred. No. 2.4e-14;	Length 439;
		1;	Mismatches 0;
		Indels 0;	Gaps 0;

OY 3 ETLMQDQORLNSWCKGRICIVYSARWH 30  
 |||||:|||||:|||||:|||||:  
 240 etlmqxnqrlnswckgricytarwh 267

RESULT 7  
 AAB12257  
 ID AAB12257 standard; peptide; 28 AA.  
 XX  
 AC AAB12257;  
 XX  
 DT 10-NOV-2000 (first entry)  
 XX  
 DE HTV-1 gp41 immunodominant region consensus sequence peptide 147 # 3.  
 XX  
 FH HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection;  
 KW acquired immunodeficiency syndrome; group O HIV; gp41.  
 XX  
 Human immunodeficiency virus type 1.  
 XX  
 PN EP1013766-A2.  
 XX  
 PD 28-JUN-2000.  
 XX  
 PF 29-NOV-1999; 99EP-0309491.  
 XX  
 PR 30-NOV-1998; 98US-0110292.  
 PR 08-FEB-1999; 99US-0119138.  
 PR 04-NOV-1999; 99US-0433428.  
 XX  
 PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.  
 XX  
 PI De Leys R, Zheng J;  
 XX  
 DR WPI; 2000-402205/35.  
 XX  
 PF New antigenic peptides and peptide functional derivatives, useful for  
 PT detection of antibodies produced in response to human immunodeficiency  
 virus group O antibodies -  
 XX  
 PS Claim 1; Page 36; 52pp; English.  
 XX  
 CC The present sequence is peptide 147-4 from Human Immunodeficiency Virus  
 CC Type 1 (HIV-1). This sequence is a partial consensus sequence of the  
 CC immunodominant region of gp41 protein derived from a variety of HIV-1  
 CC group O (outlier) strains: AN70, MV5180, VAU, DUR, POC, FAN, LOB, MAN,  
 CC NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686, ABT063, ABT124, ABT1123,  
 CC ABT2156, 193Ha, CDC7755, CDC1897, HLD28, 1515, 1516, D47-2d, HCY72c,  
 CC NF42 and PE41 (see AAB12207 to AAB1236). HIV is the principle  
 CC aetiological agent for acquired immunodeficiency syndrome (AIDS). gp41 is  
 CC used as an antigen for the detection of antibodies produced in  
 CC response to HIV infection.

XX  
 Sequence 28 AA;

Query	Match	Score	Length
Best Local Similarity	89.6%	155	DB 21;
Matches	96.4%	Pred. No. 2.5e-15;	Length 28;
		1;	Mismatches 0;
		Indels 0;	Gaps 0;

OY 3 ETLMQDQORLNSWCKGRICIVYSARWH 30  
 |||||:|||||:|||||:  
 Db 1. etlmqxnqrlnswckgricytarwh 28

RESULT 8  
 AAB12256  
 ID AAB12256 standard; peptide; 23 AA.  
 XX  
 AC AAB12256;  
 XX  
 DT 10-NOV-2000 (first entry)  
 XX  
 DE HIV-1 gp41 immunodominant region consensus sequence peptide 147-4.  
 XX  
 KW HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection;  
 KW acquired immunodeficiency syndrome; group O HIV; gp41.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN EP1013766-A2.  
 XX  
 PD 28-JUN-2000.  
 XX  
 PF 29-NOV-1999; 99EP-0309491.  
 XX  
 PR 30-NOV-1998; 98US-0110292.  
 PR 08-FEB-1999; 99US-0119138.  
 PR 04-NOV-1999; 99US-0433428.  
 XX  
 PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.  
 XX  
 PI De Leys R, Zheng J;  
 XX  
 DR WPI; 2000-402205/35.  
 XX  
 PF New antigenic peptides and peptide functional derivatives, useful for  
 PT detection of antibodies produced in response to human immunodeficiency  
 virus group O antibodies -  
 XX  
 PS Claim 1; Page 36; 52pp; English.  
 XX  
 CC The present sequence is peptide 147-4 from Human Immunodeficiency Virus  
 CC Type 1 (HIV-1). This sequence is a partial consensus sequence of the  
 CC immunodominant region of gp41 protein derived from a variety of HIV-1  
 CC group O (outlier) strains: AN70, MV5180, VAU, DUR, POC, FAN, LOB, MAN,  
 CC NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686, ABT063, ABT124, ABT1123,  
 CC ABT2156, 193Ha, CDC7755, CDC1897, HLD28, 1515, 1516, D47-2d, HCY72c,  
 CC NF42 and PE41 (see AAB12207 to AAB1236). HIV is the principle  
 CC aetiological agent for acquired immunodeficiency syndrome (AIDS). gp41 is

CC a HIV envelope protein, and so the present sequence may be used as an  
 CC antigen for the detection of antibodies produced in response to HIV  
 CC infection.  
 XX

SO Sequence 23 AA;

RESULT 9 AAB12254 standard; peptide: 23 AA.

V AAB12254; peptide: 23 AA.

X ID AAB12255 standard; peptide: 23 AA.

XK XX

AC AAB12255;

XX DT 10-NOV-2000 (first entry)

DE HIV-1 gp41 immunodominant region consensus sequence peptide 147 # 2.

KW HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection; acquired immunodeficiency syndrome; group O HIV; gp41.

XX OS Human immunodeficiency virus type 1.

XX DE HIV-1 gp41 immunodominant region consensus sequence peptide 147 # 1.

KW HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection; acquired immunodeficiency syndrome; group O HIV; gp41.

XX OS Human immunodeficiency virus type 1.

PN EPI013766-A2.

XX PR 30-NOV-1998; 98US-0110292.

XX PR 08-FEB-1999; 99US-0119138.

XX PR 04-NOV-1999; 99US-0433428.

XX PA (ORFH-) ORTHO-CLINICAL DIAGNOSTICS INC.

XX PI De Leys R, Zheng J;

XX PR 30-NOV-1999; 99EP-0309491.

XX PR 08-FEB-1999; 99US-0119138.

XX PR 04-NOV-1999; 99US-0433428.

XX DR 28-JUN-2000.

XX PI EPI013766-A2.

XX PD 28-JUN-2000.

XX PR 29-NOV-1999; 99EP-0309491.

XX PR 30-NOV-1998; 98US-0110292.

XX PR 08-FEB-1999; 99US-0119138.

XX PR 04-NOV-1999; 99US-0433428.

XX PA (ORFH-) ORTHO-CLINICAL DIAGNOSTICS INC.

XX PI De Leys R, Zheng J;

XX PR WPI; 2000-402205/35.

XX PT New antigenic peptides and peptide functional derivatives, useful for detection of antibodies produced in response to human immunodeficiency virus group O antibodies

XX PS Claim 1; Page 35; 52pp; English.

PT The present sequence is a peptide 147 related peptide from Human immunodeficiency Virus Type 1 (HIV-1). This sequence is a partial consensus sequence of the immunodominant region of gp41 protein derived from a variety of HIV-1 group O (outlier) strains: AN70, MNP180, VAU, CC POC, FAN, LOB, MAN, NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686, ABT063, ABT124, ABT123, ABT2156, 193HA, CDC1755, CDC1897, HLD28, 1515, 1516, D47-2d, HCY72C, Nr42 and PE41 (see AAB12207 to AAB1236). HIV is CC the principle aetiological agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV envelope protein, and so the present sequence may be used as an antigen for the detection of antibodies produced in CC response to HIV infection.

XX Sequence 23 AA;

Query Match 76.9%; Score 133; DB 21; Length 23;  
 Best local Similarity 95.7%; Pred. No. 2.8e-12; Length 23;  
 Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 QORLNNSWGCGKGRICLYCTSAWH 30

Db 2 qqrlnswgckgriclyctswrh 23

RESULT 11 AAB12236 standard; peptide: 33 AA.

ID AAB12236

AC AAB12236; XX  
 XX 10-NOV-2000 (first entry)  
 DT DE Partial sequence of HIV-1 strain ESS gp41 immunodominant region.  
 XX KW HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;  
 KW acquired immunodeficiency syndrome; group O HIV; gp41; ESS.  
 XX OS Human immunodeficiency virus type 1.  
 PN EP1013766-A2.  
 XX PR 28-JUN-2000.  
 XX PR 29-NOV-1999; 99EP-0309491.  
 XX PR 30-NOV-1998; 98US-0110295.  
 PR 08-FEB-1999; 99US-0119138.  
 PR 04-NOV-1999; 99US-0433428.  
 PR (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.  
 XX PI De Leys R, Zheng J;  
 DR WPI; 2000-402205/35.  
 PT New antigenic peptides and peptide functional derivatives, useful for  
 PT detection of antibodies produced in response to human immunodeficiency  
 PT virus group O antibodies -  
 PT XX Virus Type 1 (HIV-1) strain ESS. HIV is the principle aetiological  
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV  
 CC envelope protein, and may be used as an antigen for the detection of  
 CC antibodies produced in response to HIV infection. ESS is a member of  
 CC the HIV group O (outlier). The present sequence is the immunodominant region  
 CC of gp41. This sequence was used in a sequence homology alignment,  
 CC which in turn was used to derive a consensus sequence peptide: peptide  
 XX 147 (AAB12254).  
 SQ Sequence 33 AA:  
 Query Match 75.7%; Score 131; DB 21; Length 33;  
 Best Local Similarity 75.0%; Pred. No. 8.2e-12; Mismatches 2; Indels 0; Gaps 0;  
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 Oy 3 ETLMQDQQRNLSWGCKGRICYTSARWH 30  
 |||:||| |||||||:||| :|:  
 Db 6 etlilqnpqlnswgckgrivcytskwn 33  
 RESULT 12  
 AAW07343 ID AAW07343 standard; peptide; 40 AA.  
 XX AC AAW07343;  
 XX DT 03-JUN-1997 (first entry)  
 DE Partial sequence of gp41 from HIV-1 gp. O strain BCF02 (ESS).  
 XX KW Human immunodeficiency virus type 1; HIV-1; envelop; group M; group O;  
 KW C2V3-env; gp41; gag; retrovirus; strain; gp120; hypervariable loop;  
 KW primer; hybridisation; amplification; PCR; polymerase chain reaction;  
 KW immunogen; antibody.  
 XX OS Human immunodeficiency virus type 1.  
 PN W09627013-A1.  
 XX  
 XX PD 06-SEP-1996.  
 XX PR 26-FEB-1996; 96W0-FR00294.  
 XX PR 27-FEB-1995; 95FR-0002236.  
 XX PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX PI Chaix-Baudier ML, Lousset-Ajaka I, Ly T, Saragosti S, Simon F;  
 XX DR WPI; 1996-412779/41.  
 XX DR N-PSDB; AAT44918.  
 PT New strains of HIV-1 group O, related DNA fragments, peptide(s) and  
 PT antibodies - useful for diagnosis, screening and typing, or as  
 PT immunogens  
 XX PS Claim 12; Page 33; 71pp; French.  
 CC Human immunodeficiency virus type 1 (HIV-1) strains are currently  
 CC divided into 2 major groups based on the nucleotide sequences of the  
 CC envelope gene (env); group M containing sub groups A-G, and group O  
 CC containing the strains ANR70 and MPV5180. The invention relates to the  
 CC discovery of several new strains of HIV-1 which can be placed in group O,  
 CC based on the partial sequences of the C2V3-env, gp41 and gag genes (see  
 CC AAT4907-39 and AAW07329-64). The novel strains have been deposited as  
 CC retroviruses CMC1-T154 (BCF02 (ESS)), 1543 (BCF01 (FANV)), 1546 (BCF07  
 CC (MAN)), 1547 (BCF08 (NKO)) and 1545 (BCF03 (POC)). The sequence  
 CC presented here is from the strain BCF02 (ESS) and corresponds to a  
 CC fragment of the gp41 protein encoded by the env gene. The nucleic acids  
 CC can be used to detect gp O HIV-1 strains by hybridisation or (as  
 CC primers) by gene amplification, also for screening and typing of such  
 CC strains. Peptides encoded by the nucleic acids can be used as immunogens  
 CC to raise Ab for detecting gp. O HIV-1.  
 XX SQ Sequence 40 AA:  
 Query Match 75.7%; Score 131; DB 17; Length 40;  
 Best Local Similarity 75.0%; Pred. No. 1e-11; Mismatches 2; Indels 0; Gaps 0;  
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 Oy 3 ETLMQDQQRNLSWGCKGRICYTSARWH 30  
 |||:||| |||||||:||| :|:  
 Db 11 etlilqnpqlnswgckgrivcytskwn 38  
 RESULT 13  
 AAW80469 ID AAW80469 standard; peptide; 32 AA.  
 XX AC AAW80469;  
 XX DT 28-JAN-1999 (first entry)  
 DE Peptide derived from a conserved sequence of group O human HIV.  
 XX KW Group O human immune deficiency virus; HIV; detection; infection.  
 OS Synthetic.  
 OS Immune deficiency virus.  
 XX PN W09845323-A1.  
 XX PD 15-OCT-1998.  
 XX PR 06-APR-1998; 98W0-FR00691.  
 XX PR 24-FEB-1998; 98FR-0002212.  
 PR 09-APR-1997; 97FR-0004356.  
 XX

PA (SNFT ) PASTEUR SANOFI DIAGNOSTICS SA.  
 PT Cheunebaux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY;  
 XX WPI; 1998-583190/49.  
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by  
 CC human immune deficiency virus of group O  
 XX  
 PS Claim 6; Page 44; 55pp; French.  
 CC AAWW0459-74 represent synthetic peptides (either linear or cyclised by  
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences  
 CC connected around short highly conserved sequences present in isolates  
 CC of group O human immune deficiency virus (HIV). The peptides are  
 CC useful as immunological reagents for detecting infection by group O  
 CC human immune deficiency virus (HIV).  
 XX  
 SQ Sequence 32 AA;  
 Query Match 75.1%; Score 130; DB 19; Length 32;  
 Best Local Similarity 71.4%; Pred. No. 1.e-11;  
 Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 ETLMDQDQLNSNGCKGRICIVTSARWH 30  
 ||||:|||||:||||:|||||:|||||:  
 Db 3 etilinqnqdlinswgrgivcyltsvrwn 30  
 RESULT 14  
 AAB12229 ID AV67505  
 ID AAB12229 standard; peptide; 33 AA.  
 XX  
 AC AAV67606;  
 XX  
 XX  
 XX  
 DT 23-MAR-2000 (first entry)  
 DE Peptide #6 for detecting HIV-1 group O infection.  
 XX Human immunodeficiency virus-1; HIV-1; gp41 envelope protein; detection;  
 KW increased structural stability; diagnostic antigen.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9962945-A2.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 04-JUN-1999; 99WO-US12446.  
 XX  
 PR 05-JUN-1998; 98US-0088229.  
 PR 01-SEP-1998; 98US-0098705.  
 PR 15-SEP-1998; 98US-0100422.  
 PR 28-JAN-1999; 99WO-US1726.  
 XX  
 PA (PEPT-) PEPTIDE SOLUTIONS INC.  
 XX  
 PI Chowdhury MA, Bernstein D, Motsenbocker MA;  
 XX DR  
 XX  
 PT Improving properties of peptides for use as diagnostic antigens or for  
 PT preventing or treating infections -  
 XX  
 PS Claim 18; Page 61; 83pp; English.  
 XX  
 CC This peptide is derived from the human immunodeficiency virus (HIV)-1  
 CC gp41 envelope protein, and is useful for detecting HIV-1 group O  
 CC infection. The invention relates to peptides derived from HIV-1 which  
 CC have been modified for use as diagnostic antigens in the treatment or  
 CC prevention of infection. The structural stability of the peptides can be  
 CC increased in four different ways; through the replacement of a  
 CC hydrophobic amino acid with a less hydrophobic amino acid; through an  
 CC increase in the amount of secondary structure (i.e. alpha helix) in the  
 CC peptide; through the removal of a positive charge from the peptide, or  
 CC through the constraint of the epitopic sequence via the formation of a  
 CC covalent crosslink. Modified peptides of the invention are used to detect  
 CC infectious agents specifically HIV-1. Other detectable agents include  
 CC Group O viruses; human T-cell lymphotropic virus-I or -II; hepatitis C  
 CC and the causative agent of syphilis. The peptides can be used for  
 CC prevention or treatment of infections (e.g. as vaccines, or where  
 CC expressed from a transgene). More generally almost any peptide can be  
 CC similarly modified, e.g. cytokines and interferons; major  
 CC histocompatibility complex antigens; hormones; growth factors; tumour  
 CC markers or suppressors, or antigens from many other pathogens.  
 XX  
 PA (ORTH-) ORTHO-CRITICAL DIAGNOSTICS INC.  
 PT De Leyns R, Zheng J;  
 XX DR  
 XX WPI; 2000-402205/35.  
 XX  
 PT New antigenic peptides and peptide functional derivatives, useful for  
 PT detection of antibodies produced in response to human immunodeficiency  
 PT virus group O antibodies -  
 XX  
 PS Example 1; Fig 1; 52pp; English.  
 XX  
 CC The present sequence is a partial gp41 protein of Human Immunodeficiency  
 CC Virus Type 1 (HIV-1) strain HLD28. HIV is the principle aetiological  
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV  
 CC envelope protein, and may be used as an antigen for the detection of  
 CC antibodies produced in response to HIV infection. HLD28 is a member of  
 CC HIV group O (outlier). The present sequence is the immunodominant region  
 CC of gp41. This sequence was used in a sequence homology alignment,  
 CC which in turn was used to derive a consensus sequence peptide: peptide  
 CC 147 (AAB12224).  
 XX  
 SQ Sequence 33 AA;  
 Query Match 75.1%; Score 130; DB 21; Length 33;  
 Best Local Similarity 75.0%; Pred. No. 1.e-11;  
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 ETLMDQDQLNSNGCKGRICIVTSARWH 30  
 ||||:||||:|||||:|||||:  
 Db 6 etilinqnqdlinswgrgivcyltsvkwn 33

SQ Sequence 36 AA:

Query Match 75.1%; Score 130; DB 21; Length 36;  
Best Local Similarity 75.0%; Pred. No. 1. 3e-11;  
Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
OY 3 ETIAMDQORLNNSVGCKGRIICUTSARWH 30  
|||:||||| ||||:|||| :||:  
Db 8 etiliqnqqrlnlwgckgrlicytslkvn 35

Search completed: August 15, 2002, 10:46:04  
Job time: 2078 sec



Thu Aug 15 11:01:31 2002

NAME/KEY: Xaa is any amino acid  
 LOCATION: 8  
 OTHER INFORMATION: Description of Artificial Sequence:HTV Consensus  
 OTHER INFORMATION: Sequence  
 S-09-433-42BD-63

Query Match 96.0%; Score 166; DB 4; Length 30;  
 best local similarity 96.7%; Pred. No. 2.4e-18; Indels 0; Gaps 0;  
 Matches 29; Conservative 0; Mismatches 1;

GENERAL INFORMATION:  
 APPLICANT: De Leys, Robert J.  
 PATENT NO.: 6149910

FILE REFERENCE: CDS-207  
 CURRENT APPLICATION NUMBER: US/09/433,428D  
 CURRENT FILING DATE: 1999-11-04  
 NUMBER OF SEQ ID NOS: 700

SEQUENCE: ETLMODQORLNSWCKGRICLYTSARWH 30

OTHER INFORMATION: Description of Artificial Sequence:HTV Consensus  
 OTHER INFORMATION: Sequence

RESULT 3 US-09-433-42BD-67

Query Match 90.8%; Score 157; DB 4; Length 368;  
 best local similarity 96.4%; Pred. No. 3.1e-16; Indels 0; Gaps 0;  
 matches 27; conservative 1; mismatches 0;

GENERAL INFORMATION:  
 APPLICANT: Zheng, Jian  
 PATENT NO.: 6149910

FILE REFERENCE: CDS-207  
 CURRENT APPLICATION NUMBER: US/09/433,428D  
 CURRENT FILING DATE: 1999-11-04  
 NUMBER OF SEQ ID NOS: 700

SEQUENCE: ETLMODQORLNSWCKGRICLYTSARWH 30

OTHER INFORMATION: Description of Artificial Sequence:HTV Consensus  
 OTHER INFORMATION: Sequence

RESULT 4 US-09-433-42BD-67

Query Match 90.8%; Score 157; DB 4; Length 149;  
 best local similarity 96.4%; Pred. No. 3.1e-16; Indels 0; Gaps 0;  
 matches 27; conservative 1; mismatches 0;

GENERAL INFORMATION:  
 APPLICANT: De Leys, Robert J.  
 PATENT NO.: 6149910

FILE REFERENCE: CDS-207  
 CURRENT APPLICATION NUMBER: US/09/433,428D  
 CURRENT FILING DATE: 1999-11-04  
 NUMBER OF SEQ ID NOS: 700

SEQUENCE: ETLMODQORLNSWCKGRICLYTSARWH 30

OTHER INFORMATION: Description of Artificial Sequence:HTV Consensus  
 OTHER INFORMATION: Sequence

RESULT 5 US-09-433-42BD-58

Query Match 90.8%; Score 157; DB 4; Length 368;  
 best local similarity 96.4%; Pred. No. 8.5e-16; Indels 0; Gaps 0;  
 matches 27; conservative 1; mismatches 0;

GENERAL INFORMATION:  
 APPLICANT: De Leys, Robert J.  
 PATENT NO.: 6149910

FILE REFERENCE: CDS-207  
 CURRENT APPLICATION NUMBER: US/09/433,428D  
 CURRENT FILING DATE: 1999-11-04  
 NUMBER OF SEQ ID NOS: 700

SEQUENCE: ETLMODQORLNSWCKGRICLYTSARWH 30

OTHER INFORMATION: Description of Artificial Sequence:HTV Consensus  
 OTHER INFORMATION: Sequence

RESULT 6 US-09-433-42BD-57

Query Match 90.8%; Score 157; DB 4; Length 368;  
 best local similarity 96.4%; Pred. No. 8.5e-16; Indels 0; Gaps 0;  
 matches 27; conservative 1; mismatches 0;

GENERAL INFORMATION:  
 APPLICANT: De Leys, Robert J.  
 PATENT NO.: 6149910

FILE REFERENCE: CDS-207  
 CURRENT APPLICATION NUMBER: US/09/433,428D  
 CURRENT FILING DATE: 1999-11-04  
 NUMBER OF SEQ ID NOS: 700

SEQUENCE: ETLMODQORLNSWCKGRICLYTSARWH 30

OTHER INFORMATION: Description of Artificial Sequence:HTV Consensus  
 OTHER INFORMATION: Sequence

RESULT 7 US-09-433-42BD-57

Query Match 90.8%; Score 157; DB 4; Length 439;  
 best local similarity 96.4%; Pred. No. 1e-15; Indels 0; Gaps 0;  
 matches 27; conservative 1; mismatches 0;

GENERAL INFORMATION:  
 APPLICANT: De Leys, Robert J.  
 PATENT NO.: 6149910

FILE REFERENCE: CDS-207  
 CURRENT APPLICATION NUMBER: US/09/433,428D  
 CURRENT FILING DATE: 1999-11-04  
 NUMBER OF SEQ ID NOS: 700

SEQUENCE: ETLMODQORLNSWCKGRICLYTSARWH 30

OTHER INFORMATION: Description of Artificial Sequence:HTV Consensus  
 OTHER INFORMATION: Sequence

RESULT 8 US-09-433-42BD-66

Query Match 90.8%; Score 157; DB 4; Length 439;  
 best local similarity 96.4%; Pred. No. 1e-15; Indels 0; Gaps 0;  
 matches 27; conservative 1; mismatches 0;

GENERAL INFORMATION:  
 APPLICANT: De Leys, Robert J.  
 PATENT NO.: 6149910

FILE REFERENCE: CDS-207  
 CURRENT APPLICATION NUMBER: US/09/433,428D  
 CURRENT FILING DATE: 1999-11-04  
 NUMBER OF SEQ ID NOS: 700

SEQUENCE: ETLMODQORLNSWCKGRICLYTSARWH 30

OTHER INFORMATION: Description of Artificial Sequence:HTV Consensus  
 OTHER INFORMATION: Sequence

RESULT 9 US-09-433-42BD-66

Query Match 90.8%; Score 157; DB 4; Length 439;  
 best local similarity 96.4%; Pred. No. 1e-15; Indels 0; Gaps 0;  
 matches 27; conservative 1; mismatches 0;

GENERAL INFORMATION:  
 APPLICANT: De Leys, Robert J.  
 PATENT NO.: 6149910

FILE REFERENCE: CDS-207  
 CURRENT APPLICATION NUMBER: US/09/433,428D  
 CURRENT FILING DATE: 1999-11-04  
 NUMBER OF SEQ ID NOS: 700

SEQUENCE: ETLMODQORLNSWCKGRICLYTSARWH 30

OTHER INFORMATION: Description of Artificial Sequence:HTV Consensus  
 OTHER INFORMATION: Sequence

RESULT 10 US-09-433-42BD-66

Query Match 90.8%; Score 157; DB 4; Length 439;  
 best local similarity 96.4%; Pred. No. 1e-15; Indels 0; Gaps 0;  
 matches 27; conservative 1; mismatches 0;

GENERAL INFORMATION:  
 APPLICANT: De Leys, Robert J.  
 PATENT NO.: 6149910

FILE REFERENCE: CDS-207  
 CURRENT APPLICATION NUMBER: US/09/433,428D  
 CURRENT FILING DATE: 1999-11-04  
 NUMBER OF SEQ ID NOS: 700

SEQUENCE: ETLMODQORLNSWCKGRICLYTSARWH 30

OTHER INFORMATION: Description of Artificial Sequence:HTV Consensus  
 OTHER INFORMATION: Sequence

Sequence 62; Application US/09433428D  
; Patent No. 6149910  
; GENERAL INFORMATION:  
; APPLICANT: De Leys, Robert J.  
; INVENTOR: Zheng, Jian  
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
; FILE REFERENCE: CDS-207  
; CURRENT APPLICATION NUMBER: US/09/433,428D  
; CURRENT FILING DATE: 1999-11-04  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 62  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: xaa is any amino acid  
; LOCATION: 6  
; OTHER INFORMATION: Description of Artificial sequence:HIV Consensus  
; US-09-433-428D-62

Query Match Similarity 89.6%; Score 155; DB 4; Length 35;  
Best Local Similarity 96.4%; Pred. No. 1e-16; Matches 27; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
US-09-433-428D-64  
; Sequence 64, Application US/09433428D  
; Patent No. 6149910  
; GENERAL INFORMATION:  
; APPLICANT: De Leys, Robert J.  
; INVENTOR: Zheng, Jian  
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
; FILE REFERENCE: CDS-207  
; CURRENT APPLICATION NUMBER: US/09/433,428D  
; CURRENT FILING DATE: 1999-11-04  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: xaa is any amino acid  
; LOCATION: 13  
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus  
; US-09-433-428D-64

Query Match Similarity 89.6%; Score 155; DB 4; Length 35;  
Best Local Similarity 96.4%; Pred. No. 1.3e-16; Matches 27; Conservatve 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 8  
US-09-433-428D-64  
; Sequence 64, Application US/09433428D  
; Patent No. 6149910  
; GENERAL INFORMATION:  
; APPLICANT: De Leys, Robert J.  
; INVENTOR: Zheng, Jian  
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
; FILE REFERENCE: CDS-207  
; CURRENT APPLICATION NUMBER: US/09/433,428D  
; CURRENT FILING DATE: 1999-11-04  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 62  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: xaa is any amino acid  
; LOCATION: 6  
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus  
; US-09-433-428D-62

Query Match Similarity 77.5%; Score 134; DB 4; Length 23;  
Best Local Similarity 95.7%; Pred. No. 1.1e-13; Matches 22; Conservatve 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 10  
US-09-433-428D-59  
; Sequence 59, Application US/09433428D  
; Patent No. 6149910  
; GENERAL INFORMATION:  
; APPLICANT: De Leys, Robert J.  
; INVENTOR: Zheng, Jian  
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
; FILE REFERENCE: CDS-207  
; CURRENT APPLICATION NUMBER: US/09/433,428D  
; CURRENT FILING DATE: 1999-11-04  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: xaa is any amino acid  
; LOCATION: 13  
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus  
; US-09-433-428D-59

Query Match Similarity 76.9%; Score 133; DB 4; Length 23;  
Best Local Similarity 95.7%; Pred. No. 1.6e-13; Matches 22; Conservatve 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 11  
US-09-433-428D-60  
; Sequence 60, Application US/09433428D  
; Patent No. 6149910  
; GENERAL INFORMATION:  
; APPLICANT: De Leys, Robert J.  
; INVENTOR: Zheng, Jian  
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
; FILE REFERENCE: CDS-207  
; CURRENT APPLICATION NUMBER: US/09/433,428D  
; CURRENT FILING DATE: 1999-11-04  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 60  
; LENGTH: 23  
; TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: NAME/KEY: xaa is any amino acid

LOCATION: 1

OTHER INFORMATION: Description of Artificial Sequence: HIV consensus

; US-09-433-428D-60

Query Match 76.3%; score 132; DB 4; Length 23;

Best Local Similarity 100.0%; Pred. No. 2.2e-13; Mismatches 0; Indels 0; Gaps 0; Matches 22; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 9 QQRNLNSWGCKGRICITYTSARWH 30

Db 2 QQRNLNSWGCKGRICITYTSARWH 23

GENERAL INFORMATION:

APPLICANT: De Leys, Robert J.

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

PATENT NO.: 6149910

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 30

LENGTH: 33

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

; US-09-433-428D-30

Query Match 75.7%; Score 131; DB 4; Length 33;

Best Local Similarity 75.0%; Pred. No. 4.6e-13; Mismatches 5; Indels 0; Gaps 0; Matches 21; Conservative 2; MisMatches 0; Indels 0; Gaps 0;

QY 3 ETLMDQDQRNLNSWGCKGRICITYTSARWH 30

Db 6 ETLLQDQNLNSWGCKGRIVCVNSVKWN 33

RESULT 13

Sequence 35, Application US/08894699

PATENT NO. 6030769

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: SARAGOSTI, SENTOB

APPLICANT: LOUSSERT-AJAKA, IBITISSAM

APPLICANT: LY, THOAI-DUONG

APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

APPLICANT: LOUSSERT-AJAKA, IBITISSAM

APPLICANT: LY, THOAI-DUONG

APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAYER & NEUSTADT, P.C.

ADDRESS: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

STREET: FLOR CITY: ARLINGTON

CITY: ARLINGTON STATE: VA

ZIP: 22202 COUNTRY: USA

COMPUTER READABLE FORM: COMPUTER: IBM PC compatible

MEDIUM TYPE: FLOPPY disk OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

RESULT 14

US-09-444-410-36

Sequence 36, Application US/09444410

PATENT NO. 6270975

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS

APPLICANT: LOUSSERT-AJAKA, IBITISSAM

APPLICANT: LY, THOAI-DUONG

APPLICANT: CHAIX-BAUDIER, MARIE-LAURE

TITLE OF INVENTION: VIRUSES, AND USES THEREOF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAYER & NEUSTADT, P.C.

ADDRESS: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH

STREET: FLOR CITY: ARLINGTON

CITY: ARLINGTON STATE: VA

ZIP: 22202 COUNTRY: USA

COMPUTER READABLE FORM: COMPUTER: IBM PC compatible

MEDIUM TYPE: FLOPPY disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/444,410

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95/02236

;  
 ; FILING DATE: 27-FEB-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: OBLON, NORMAN F.  
 ; REGISTRATION NUMBER: 24,614  
 ; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 703-413-3000  
 ; TELEFAX: 703-413-2220  
 ; INFORMATION FOR SEQ ID NO: 36:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 40 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLogy: linear  
 ; MOLECULE TYPE: peptide  
 ; US-09-444-410-36

Query Match, 75.7%; Score 131; DB 4; Length 40;  
 Best Local Similarity 75.0%; Pred. No. 5.7e-13;  
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 Qy 3 ETLMDQDQRNLNSWCKGRICIVTSARWH 30  
 Db 11 ETLIONQDQIINNSWCKGRICIVTSVKWN 38

## RESULT 15

US-09-433-428D-23  
 ; Sequence 23, Application US/09433428D  
 ; Patent No. 6149910  
 ; GENERAL INFORMATION:  
 ; APPLICANT: De Ley, Robert J.  
 ; APPLICANT: Zheng, Jian  
 ; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O  
 ; FILE REFERENCE: CDS-207  
 ; CURRENT APPLICATION NUMBER: US/09/433,428D  
 ; CURRENT FILING DATE: 1999-11-04  
 ; NUMBER OF SEQ ID NOS: 70  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 23  
 ; LENGTH: 33  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus type 1  
 ; US-09-433-428D-23

Query Match, 75.1%; Score 130; DB 4; Length 33;  
 Best Local Similarity 75.0%; Pred. No. 6.5e-13; Length 33;  
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 Qy 3 ETLMDQDQRNLNSWCKGRICIVTSARWH 30  
 Db 6 ETLMONQDQIINNSWCKGRICIVTSVKWN 33

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<b>OM protein - protein search, using sw model</b>									
Run on: August 15, 2002, 10:41:11 ; Search time 15.15 Seconds (without alignments) 190.276 Million cell updates/sec									
<b>Title:</b> Perfect score: <b>Sequence:</b> US-09-605-573A-69 <b>Scoring table:</b> BLOSUM62 <b>Searched:</b> Gapop 10.0 , Gapext 0.5									
Total number of hits satisfying chosen parameters: 283138									
Minimum DB seq length: 0 Maximum DB seq length: 2000000000									
<b>Post-processing:</b> Minimum Match 0% Maximum Match 100% Listing first 45 summaries									
<b>Database :</b> PIR_71;* 1: PIR1;* 2: P12;* 3: P13;* 4: PIR4;*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
<b>SUMMARIES</b>									
Result No.	Score	Query Match Length	DB ID	Description	RESULT	1	ALIGNMENTS		
1	118	68.2	104	2 S52930	S52930				
2	116	67.1	863	2 A53034	GP41 ENV protein -	C;Species: human immunodeficiency virus type 1, HIV-1			
3	114	65.9	877	2 S49197	gag polyprotein -	C;Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999			
4	93	53.8	854	1 VCLJH1	env envelope protein p	C;Accession: S52930			
5	92	53.2	858	1 VCLJG2	env polyprotein pr	R;Cohen, J.H.M.; Guetard, D.; Philbert, F.; Charnare, S.; Tabary, T.; Montagnier, L.			
6	89	51.4	864	1 VCLJG4	env polyprotein pr	submitted to the EMBL Data Library, January 1995			
7	88	50.9	357	2 S21990	env polyprotein -	A;Description: A novel HIV-1 strain illustrates the diversity of the O group.			
8	88	50.9	358	2 S22000	envelope protein g	A;Reference number: S52929			
9	87	50.3	358	2 S22000	envelope protein g	A;Accession: S52930			
10	87	50.3	358	2 S70417	envelope protein g	A;Status: preliminary			
11	87	50.3	859	1 VCLJST	env polyprotein pr	A;Molecule type: genomic RNA			
12	86	49.7	151	2 S30448	env polyprotein -	A;Residues: 1-104 <COH>			
13	86	49.7	151	2 S30453	env envelope protein g	A;Cross-references: EMBL:X84328; NID:9695526; PID:9695527			
14	86	49.7	151	2 S30452	env envelope protein g	C;Superfamily: type E retrovirus env polyprotein			
15	86	49.7	151	2 S30450	env envelope protein g	C;Keywords: polyprotein			
16	86	49.7	151	2 S30451	env envelope protein g				
17	86	49.7	856	1 A44963	env envelope protein g				
18	85	49.1	151	2 S30457	env envelope protein g				
19	85	49.1	151	2 S30456	env envelope protein g				
20	85	49.1	151	2 S30455	env envelope protein g				
21	85	49.1	151	2 S30454	env envelope protein g				
22	85	49.1	357	2 S22006	env envelope protein g				
23	85	49.1	357	2 S21994	env envelope protein g				
24	85	49.1	357	2 S22004	env envelope protein g				
25	85	49.1	357	2 S21995	env envelope protein g				
26	85	49.1	357	2 S21992	env envelope protein g				
27	85	49.1	358	2 S21998	env envelope protein g				
28	85	49.1	443	2 C16121	env envelope protein g				
29	85	49.1	445	2 A1621	env envelope protein M				
Query Match 67.1%; Score 116; DB 2; Length 863; Best Local Similarity 60.7%; Pred. No. 1.7e-08; Matches 17; Conservative 8; Mismatches 3; Indels 0; Gaps 0;									
OY	3	ETLMQDQORLNNSWGCKGRICITYTSARWH	30						

	RESULT	3
S49197		
C;Envelope: protein precursor - human immunodeficiency virus type 1 (fragment)		
C;Species: human immunodeficiency virus type 1, HIV-1		
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999		
C;Accession: S49197		
R;Charneau, P.; Borman, A.M.; Quillett, C.; Guetard, D.; Chamaret, S.; Cohen, J.; Remy, submitted to the EMBL Data Library, July 1994		
A;Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: definition and organization of the genome		
A;Reference number: S49197		
A;Accession: S49197		
A;Residues: 1-877 <CHA>		
A;Molecule type: DNA		
A;Cross-references: EMBL:X80020; NID:9510516; PIDN:CAA56323.1; PID:9510517		
A;Experimental source: isolate VAU		
C;Superfamily: type E retrovirus env polyprotein		
C;Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein		
C;1-30/Domain: signal sequence #status predicted <SIG>		
C;31-535/Product: coat protein gp120 #status predicted <CP1>		
F;526-877/Product: coat protein gp41 #status predicted <CP2>		
F;598-716/Domain: transmembrane #status predicted <TMN>		
F;599-887,39,148,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,404,599,887,39,148,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,404,		
Query Match Similarity 65.9%; Score 114; DB 2; Length 877;		
Best Local Similarity 64.3%; Pred. No. 3.3e-08; Mismatches 5; Indels 0; Gaps 0;		
Matches 18; Conservative 5; Mismatches 5; Indels 0; Gaps 0;		
QY 3 ETLMDOQORLNSWGGKGRICITYSARWH 30		
Db 599 ETFIQNOQLINLWGCKNRILCITYSVKW 626		
RESULT	4	
VCLJSTI		
env polyprotein precursor - simian immunodeficiency virus SIVcpz		
N;Alternate names: coat polyprotein		
N;Contains: coat protein gp120; coat protein gp41		
C;Species: simian immunodeficiency virus SIVcpz		
A;Note: host Pan troglodytes (chimpanzee)		
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999		
C;Accession: S09990		
R;Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.		
Nature 345, 356-359, 1990		
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.		
A;Reference number: S09983; MUID:90259077		
A;Accession: S09990		
A;Status: nucleic acid sequence not shown; translation not shown		
A;Molecule type: DNA		
A;Residues: 1-854 <HUE>		
A;Cross-references: EMBL:X52154; NTB:958866; PIDN:CAA36407.1; PID:958874		
C;Genetics:		
A;Gene: env		
C;Superfamily: type E retrovirus env polyprotein		
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein		
F;1-30/Domain: signal sequence #status predicted <SIG>		
F;31-500/Product: coat protein gp120 #status predicted <CP1>		
F;501-854/Product: coat protein gp41 #status predicted <CP2>		
F;501-517/Domain: transmembrane #status predicted <TM1>		
F;675-693/Domain: transmembrane #status predicted <TM2>		
F;805-821/Domain: transmembrane #status predicted <TM3>		
F;134,140,143,154,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45		
Query Match Similarity 53.8%; Score 93; DB 1; Length 854;		
Best Local Similarity 50.0%; Pred. No. 3.2e-05; Mismatches 9; Indels 0; Gaps 0;		
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;		
QY 3 ETLMDOQORLNSWGGKGRICITYSARWH 30		
Db 608 EKYLEDQARLNLSWGCACWKVCHTVEW 634		
RESULT	5	
VCLJSG2		
env polyprotein precursor - human immunodeficiency virus type 2 (isolate ROD)		
N;Alternate names: coat polyprotein		
C;Species: human immunodeficiency virus type 2, HIV-2		
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999		
C;Accession: C26262		
R;Guaderrama, M.; Emerman, M.; Sonigo, P.; Clavel, F.; Montagnier, L.; Alizon, M.		
Nature 266, 662-669, 1987		
A;Title: Genome organization and transactivation of the human immuno-deficiency virus		
A;Reference number: R26262; MUID:87173056		
A;Contents: proviral DNA		
A;Accession: C26262		
A;Molecule type: DNA		
A;Residues: 1-558 <GIV>		
A;Cross-references: GB:MI5390; NID:91332361; PIDN:AAB00770.1; PID:9325749		
A;Genetics:		
A;Gene: env		
C;Superfamily: type E retrovirus env polyprotein		
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein		
F;1-11/Domain: signal sequence #status predicted <SIG>		
F;18-858/Product: env Polyprotein #status predicted <MAT>		
F;18-858/Product: exterior membrane glycoprotein #status predicted <EXT>		
F;18-501/Product: transmembrane glycoprotein #status predicted <TM>		
F;18-858/Product: transmembrane glycoprotein #status predicted <TM>		
F;34,67,76,119,120,151,166,179,192,193,196,206,238,241,248,272,278,289,300,367,371,40		
Query Match Similarity 53.2%; Score 92; DB 1; Length 858;		
Best Local Similarity 55.6%; Pred. No. 4.4e-05; Mismatches 8; Indels 0; Gaps 0;		
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;		
QY 3 ETLMDOQORLNSWGGKGRICITYSARWH 29		
Db 583 EKYLQDGARLNLSWGCACWKVCHTVEW 609		
RESULT	6	
VCLJG4		
env polyprotein - simian immunodeficiency virus (African green monkey isolate)		
C;Species: simian immunodeficiency virus, SIV		
C;Date: 30-Jun-1998 #sequence_revision 30-Jun-1998 #text_change 24-Oct-1997		
C;Accession: G30045		
R;Fukasawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Miki, K.; Kitahara, Nature 333, 457-461, 1988		
A;Title: Sequence of simian immunodeficiency virus from African green monkey, a new		
A;Reference number: A30045; MUID:88232906		
A;Accession: G30045		
A;Molecule type: DNA		
A;Residues: 1-864 <FKU>		
A;Cross-references: EMBL:X07805		
C;Genetics:		
A;Gene: env		
C;Superfamily: type E retrovirus env polyprotein		
C;Keywords: AIDS; capsid protein; coat protein; immunodeficiency; polyprotein; trans		
Query Match Similarity 51.4%; Score 89; DB 1; Length 864;		
Best Local Similarity 48.1%; Pred. No. 0.00012; Mismatches 8; Indels 0; Gaps 0;		
Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;		
QY 3 ETLMDOQORLNSWGGKGRICITYSARWH 29		
Db 608 EKYLEDQARLNLSWGCACWKVCHTVEW 634		
RESULT	7	
S21990		
envelope protein gp120/gp41 - human immunodeficiency virus type 1		
C;Species: human immunodeficiency virus type 1, HIV-1		
A;Variety: isolate 20		

C; Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C; Accession: S21990; S70423  
 R; Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 A; Submitted to the EMBL Data Library, July 1991  
 A; Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by sequencing of gp120/gp41  
 A; Reference number: S21990  
 A; Accession: S21990  
 A; Molecule type: DNA  
 A; Residues: 1-357 <STE1>  
 A; Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176  
 A; Reference number: S70423  
 A; Accession: S70423  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-332, 'X', 334-357 <STE2>  
 C; Superfamily: type E retrovirus env polyprotein

RESULT 8  
 S22002  
 Best Local Similarity 50.9%; Score 88; DB 2; Length 357;  
 Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;  
 C; Species: human immunodeficiency virus type 1, HIV-1  
 A; Variety: isolate 3L  
 C; Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C; Accession: S22002; S70418  
 R; Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 A; Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by sequencing of gp120/gp41  
 A; Reference number: S21990  
 A; Molecule type: DNA  
 A; Residues: 1-358 <STE1>  
 A; Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43616.1; PID:960187  
 R; Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A; Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by sequencing of gp120/gp41  
 A; Reference number: S70417; MID:92144209  
 A; Accession: S70418  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-333, 'X', 335-358 <STE2>  
 A; Cross-references: EMBL:X61352; NID:960186  
 C; Superfamily: type E retrovirus env polyprotein

RESULT 10  
 S70417  
 Best Local Similarity 50.3%; Score 87; DB 2; Length 358;  
 Matches 14; Conservative 4; Mismatches 10; Indels 0; Gaps 0;  
 C; Species: human immunodeficiency virus type 1 (patient 3B) (fragment)  
 A; Variety: patient 3B  
 C; Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 26-Aug-1999  
 C; Accession: S70417  
 R; Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A; Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by sequencing of gp120/gp41  
 A; Reference number: S70417; MID:92144209  
 A; Accession: S70417  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-358 <STE>  
 A; Cross-references: EMBL:X61351; NID:960184; PIDN:CAA43614.1; PID:960185  
 C; Superfamily: type E retrovirus env polyprotein

RESULT 11  
 VCLJST  
 Best Local Similarity 50.3%; Score 87; DB 2; Length 358;  
 Matches 14; Conservative 4; Mismatches 10; Indels 0; Gaps 0;  
 C; Species: human immunodeficiency virus type 2 (isolate ST)  
 N; Contains: surface glycoprotein gp120; transmembrane glycoprotein gp41  
 C; Note: host Homo sapiens (man)  
 C; Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Sep-1994  
 C; Accession: H33943  
 R; Kumar, P.; Hui, H.; Kappes, J.C.; Haggerty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G.  
 J. Virol. 64, 890-901, 1990  
 A; Title: Molecular characterization of an attenuated human immunodeficiency virus type 2  
 A; Reference number: A33943; MID:90112662  
 A; Accession: H33943  
 A; Molecule type: genomic RNA  
 A; Residues: 1-859 <KUM>  
 A; Cross-references: EMBL:M86924  
 C; Genetics:  
 A; Gene: env  
 C; Superfamily: type E retrovirus env polyprotein  
 C; Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F; 1-19/Domain: signal sequence #status predicted <SGG>  
 F; 20-859/Product: env polyprotein #status predicted <ENV>  
 F; 20-501/Product: surface glycoprotein gp120 #status predicted <SGG>

RESULT 9  
 S22000  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C; Species: human immunodeficiency virus type 1, HIV-1  
 C; Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 12-Apr-1995  
 C; Accession: S22000

F;506-859#product: transmembrane glycoprotein gp41 #status predicted <TGG>  
 F;507-523#Region: hydrophobic  
 F;675-694#Domain: transmembrane #status predicted <TMN>  
 F;36,69,78,113,119,131,137,145,160,173,186,200,232,235,242,266,272,283,294,304,359,392,400  
 Query Match 50.3%; Score 87; DB 1; Length 859;  
 Best Local Similarity 48.1%; Pred. No. 0.00023; 8; Mismatches 6; Indels 0; Gaps 0;  
 Matches 13; Conservative 6;  
 QY 3 ETLMQDQRINNSWGCKGRICIVTSARW 29  
 Db 577 EKYLKDQAQLNSWGCAFRQVCHITVW 603

RESULT 12

S30448 Query Match 50.3%; Score 87; DB 1; Length 859;  
 C;Species: human immunodeficiency virus type 2, HIV-2  
 C;Date: 02-Dec-1993 #sequence\_revision 30-Jan-1998 #text\_change 17-Mar-1999  
 A;Accession: S30448; S30449; S30481; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;  
 R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;  
 Nature 358, 495-499, 1992  
 A;Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.  
 A;Reference number: S30448; MUID:92350299  
 A;Accession: S30448  
 A;Molecule type: nucleic acid  
 A;Residues: 1-151 <GAO>  
 A;Cross-references: EMBL:M87069  
 A;Experimental source: FOENVA13  
 A;Accession: S30449  
 A;Status: preliminary; translation not shown  
 A;Molecule type: nucleic acid  
 A;Residues: 1-151 <GAZ>  
 A;Cross-references: EMBL:M87071  
 A;Experimental source: FOENVA3  
 R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;  
 submitted to the EMBL Data Library, December 1992  
 A;Description: Human infection by genetically diverse SIV(SM)-related HIV-2 in west Africa  
 A;Reference number: S30460  
 A;Accession: S30480  
 A;Status: preliminary  
 A;Molecule type: nucleic acid  
 A;Residues: 1-151 <GA2>  
 A;Cross-references: EMBL:M87085  
 A;Accession: S30481  
 A;Status: preliminary  
 A;Molecule type: nucleic acid  
 A;Residues: 1-151 <GA3>  
 A;Cross-references: EMBL:M87076  
 C;Genetics:  
 A;Gene: env  
 C;Superfamily: type E retrovirus env polyprotein  
 C;Keywords: coat protein; glycoprotein

C;Keywords: coat protein; glycoprotein

Query Match 49.7%; Score 86; DB 2; Length 151;  
 Best Local Similarity 48.1%; Pred. No. 6.2e-05; 6; Mismatches 8; Indels 0; Gaps 0;  
 Matches 13; Conservative 6;  
 QY 3 ETLMQDQRINNSWGCKGRICIVTSARW 29  
 Db 28 EKYLKDQAQLNSWGCAFRQVCHITVW 54

RESULT 14

S30452 Query Match 49.7%; Score 86; DB 2; Length 151;  
 C;Species: human immunodeficiency virus type 2, HIV-2  
 C;Date: 02-Dec-1993 #sequence\_revision 30-Jan-1998 #text\_change 17-Mar-1999  
 C;Accession: S30452  
 R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;  
 Nature 358, 495-499, 1992  
 A;Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.  
 A;Reference number: S30448; MUID:92350299  
 A;Accession: S30452  
 A;Molecule type: nucleic acid  
 A;Residues: 1-151 <GAO>  
 A;Cross-references: EMBL:M87075  
 A;Experimental source: FOENVA3  
 R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;  
 submitted to the EMBL Data Library, December 1992  
 A;Description: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.  
 A;Reference number: S30460  
 A;Accession: S30480  
 A;Status: preliminary  
 A;Molecule type: nucleic acid  
 A;Residues: 1-151 <GA2>  
 A;Cross-references: EMBL:M87085  
 A;Accession: S30481  
 A;Status: preliminary  
 A;Molecule type: nucleic acid  
 A;Residues: 1-151 <GA3>  
 A;Cross-references: EMBL:M87076  
 C;Genetics:  
 A;Gene: env  
 C;Superfamily: type E retrovirus env polyprotein  
 C;Keywords: coat protein; glycoprotein

C;Keywords: coat protein; glycoprotein

Query Match 49.7%; Score 86; DB 2; Length 151;  
 Best Local Similarity 48.1%; Pred. No. 6.2e-05; 6; Mismatches 8; Indels 0; Gaps 0;  
 Matches 13; Conservative 6;  
 QY 3 ETLMQDQRINNSWGCKGRICIVTSARW 29  
 Db 28 EKYLKDQAQLNSWGCAFRQVCHITVW 54

RESULT 15

S30450 Query Match 49.7%; Score 86; DB 2; Length 151;  
 C;Species: human immunodeficiency virus type 2, HIV-2  
 C;Date: 02-Dec-1993 #sequence\_revision 30-Jan-1998 #text\_change 17-Mar-1999  
 C;Accession: S30450  
 R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;  
 Nature 358, 495-499, 1992  
 A;Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.  
 A;Reference number: S30448; MUID:92350299  
 A;Accession: S30450  
 A;Status: translation not shown  
 A;Molecule type: nucleic acid  
 A;Residues: 1-151 <GAO>  
 A;Cross-references: EMBL:M87072  
 C;Genetics:  
 A;Gene: env  
 C;Superfamily: type E retrovirus env polyprotein  
 C;Keywords: coat protein; glycoprotein

C;Keywords: coat protein; glycoprotein

Query Match 50.3%; Score 87; DB 1; Length 859;  
 Best Local Similarity 48.1%; Pred. No. 0.00023; 8; Mismatches 6; Indels 0; Gaps 0;  
 Matches 13; Conservative 6;  
 QY 3 ETLMQDQRINNSWGCKGRICIVTSARW 29  
 Db 28 EKYLKDQAQLNSWGCAFRQVCHITVW 54

RESULT 13

S30453 Query Match 50.3%; Score 87; DB 1; Length 859;  
 C;Species: human immunodeficiency virus type 2, HIV-2  
 C;Date: 02-Dec-1993 #sequence\_revision 30-Jan-1998 #text\_change 17-Mar-1999  
 C;Accession: S30453  
 R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;  
 Nature 358, 495-499, 1992

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Query Match 49.7%; Score 86; DB 2; Length 151;  
Best Local Similarity 48.1%; Pred. No. 6.2e-05;  
Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
QY 3 ETLMQDQQRINNSWCKGRITCYSARW 29  
Db 28 EKVLRKDQAGINSWCAFRQVCHTIVW 54

Search completed: August 15, 2002, 10:46:45  
Job time: 334 sec

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PT	CARBHYD	119	119	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	HIV: X07805; ENV\$AGMTY.
PT	CARBHYD	120	120	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	InterPro: IPR00328; Env_GP41.
PT	CARBHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	IntraPro: IPR00777; GP120.
PT	CARBHYD	166	166	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	pFan: PF00516; GP120; 1.
PT	CARBHYD	179	179	N-LINKED (GLCNAC. . .) (POTENTIAL).	KW	AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
PT	CARBHYD	192	192	N-LINKED (GLCNAC. . .) (POTENTIAL).	KW	Signal.
FT	CARBHYD	193	193	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	SIGNAL
FT	CARBHYD	196	196	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	1
FT	CARBHYD	206	206	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	20
FT	CARBHYD	238	238	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	POTENTIAL.
FT	CARBHYD	241	241	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	EXTEIOR MEMBRANE GLYCOPROTEIN.
FT	CARBHYD	248	248	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	TRANSMEMBRANE GLYCOPROTEIN.
FT	CARBHYD	272	272	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	IN- FRAME TERMINATION CODON.
FT	CARBHYD	278	278	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	TERMINATION CODON.
FT	CARBHYD	289	289	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBOHYD
FT	CARBHYD	300	300	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	770
FT	CARBHYD	310	310	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	35
FT	CARBHYD	367	371	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBHYD
FT	CARBHYD	400	400	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	68
FT	CARBHYD	410	410	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	68
FT	CARBHYD	447	447	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	17
FT	CARBHYD	463	466	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	117
FT	CARBHYD	611	611	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	150
FT	CARBHYD	620	620	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	150
FT	CARBHYD	636	636	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	155
FT	CONFLICT	312	312	T -> I (IN REF. 1; AAB00770).	FT	165
SO	SEQUENCE	858	AA;	858 AA; MW: C7266AF1F5C5B9A7 CRC64;	FT	195
Query Match	53.2%	Score 92;	DB 1;	Length 858;	FT	198
Best Local Similarity	55.6%	Pred. No.	3.9e-06;		FT	210
Matches	15;	Conservative	4;	Mismatches 8;	FT	210
Indels	0;	Gaps	0;		FT	252
OQ	3 ETLMDQDQRQLNSWGWGCAFQVCHTTVPM 609	Db	583 EKYLQDQARLNNSWGWGCAFQVCHTTVPM 609		FT	252
RESULT 4	ENV_SIVAT	STANDARD:	PRT:	865 AA.	FT	255
ID	ENV_SIVAT	STANDARD:	PRT:	865 AA.	FT	255
AC	P05866;				FT	255
DT	01-Nov-1988 (Rel. 09, Created)				FT	255
DT	01-Nov-1988 (Rel. 09, Last sequence update)				FT	255
DE	Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				FT	255
DE	Env. Simian immunodeficiency virus (TYS-1 isolate) (SIV-AGM).				FT	255
DE	Viruses; Retroviridae; Lentivirus.				FT	255
[1]	"Sequence of simian immunodeficiency virus from African green monkey, a new member of the HIV/SIV group."				FT	255
RL	Nature 33:457-461(1988).				FT	255
RX	MEDLINE=8823906; PubMed=374586;				FT	255
RA	Fukazawa M., Miura T., Hasegawa A., Morikawa S., Tsujimoto H.,				FT	255
RA	Miki K., Kitamura T., Hayami M.,				FT	255
RA	"Sequence of simian immunodeficiency virus from African green monkey,"				FT	255
RA	the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).				FT	255
DR	EMBL: X07805; CAA30663.2; -				FT	255
DR	PIR: G30045; VCLJG4.				FT	255
Query Match	51.4%	Score 89;	DB 1;	Length 865;	DR	HIV: X07805; ENV\$AGMTY.
Best Local Similarity	54.1%	Pred. No.	1.1e-05;		DR	InterPro: IPR00328; Env_GP41.
Matches	13;	Conservative	6;	Mismatches 8;	DR	IntraPro: IPR00777; GP120.
Indels	0;	Gaps	0;		DR	pFan: PF00516; GP120; 1.
OQ	3 ETLMDQDQRQLNSWGWGCAFQVCHTTVPM 634	Db	608 EKYLQDQARLNNSWGWGCAFQVCHTTVPM 634		DR	AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
RESULT 5	ENV_SIVAT	STANDARD:	PRT:	854 AA.	DR	Signal.
ID	ENV_SIVAT	STANDARD:	PRT:	854 AA.	DR	SIGNAL
AC	Q02837;				DR	1
DT	01-JUL-1993 (Rel. 26, Created)				DR	POTENTIAL.
DT	01-JUL-1993 (Rel. 26, Last sequence update)				DR	EXTEIOR MEMBRANE GLYCOPROTEIN.
DT	16-OCT-2001 (Rel. 40, Last annotation update)				DR	TRANSMEMBRANE GLYCOPROTEIN.
DE	Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				DR	IN- FRAME TERMINATION CODON.
DE	Env. Simian immunodeficiency virus (Isolate AGM / clone GRI-1) (SIV-AGM).				DR	TERMINATION CODON.
DE	Viruses; Retroviridae; Lentivirus.				DR	CARBOHYD
[1]	NCBI_TAXID=31694;				DR	770
RN	SEQUENCE FROM N.A.				DR	35
RN	SEQUENCE FROM N.A.				DR	CARBHYD
RX	MEDLINE=9122660; PubMed=2024476;				DR	35
RA	Forsberg A., Hirsch V.M., Allan J.S., Johnson P.R.;				DR	CARBHYD
RA	"A highly divergent proviral DNA clone of SIV from a distinct species of African green monkey";				DR	35
RA	Virology 182:397-402(1991).				DR	CARBHYD
RA	-1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.				DR	35
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CC	EMBL: X07805; CAA30663.2; -				DR	35
CC	PIR: G30045; VCLJG4.				DR	35
Query Match	51.4%	Score 89;	DB 1;	Length 865;	DR	HIV: X07805; ENV\$AGMTY.
Best Local Similarity	54.1%	Pred. No.	1.1e-05;		DR	InterPro: IPR00328; Env_GP41.
Matches	13;	Conservative	6;	Mismatches 8;	DR	IntraPro: IPR00777; GP120.
Indels	0;	Gaps	0;		DR	pFan: PF00516; GP120; 1.
OQ	3 ETLMDQDQRQLNSWGWGCAFQVCHTTVPM 634	Db	608 EKYLQDQARLNNSWGWGCAFQVCHTTVPM 634		DR	AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
RESULT 6	ENV_SIVAT	STANDARD:	PRT:	854 AA.	DR	Signal.
ID	ENV_SIVAT	STANDARD:	PRT:	854 AA.	DR	SIGNAL
AC	Q02837;				DR	1
DT	01-JUL-1993 (Rel. 26, Created)				DR	POTENTIAL.
DT	01-JUL-1993 (Rel. 26, Last sequence update)				DR	EXTEIOR MEMBRANE GLYCOPROTEIN.
DT	16-OCT-2001 (Rel. 40, Last annotation update)				DR	TRANSMEMBRANE GLYCOPROTEIN.
DE	Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				DR	IN- FRAME TERMINATION CODON.
DE	Env. Simian immunodeficiency virus (Isolate AGM / clone GRI-1) (SIV-AGM).				DR	TERMINATION CODON.
DE	Viruses; Retroviridae; Lentivirus.				DR	CARBOHYD
[1]	NCBI_TAXID=31694;				DR	770
RN	SEQUENCE FROM N.A.				DR	35
RN	SEQUENCE FROM N.A.				DR	CARBHYD
RX	MEDLINE=9122660; PubMed=2024476;				DR	35
RA	Forsberg A., Hirsch V.M., Allan J.S., Johnson P.R.;				DR	35
RA	"A highly divergent proviral DNA clone of SIV from a distinct species of African green monkey";				DR	35
RA	Virology 182:397-402(1991).				DR	35
RA	-1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.				DR	35
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).				DR	35
CC	EMBL: X07805; CAA30663.2; -				DR	35
CC	PIR: G30045; VCLJG4.				DR	35
Query Match	51.4%	Score 89;	DB 1;	Length 865;	DR	HIV: X07805; ENV\$AGMTY.
Best Local Similarity	54.1%	Pred. No.	1.1e-05;		DR	InterPro: IPR00328; Env_GP41.
Matches	13;	Conservative	6;	Mismatches 8;	DR	IntraPro: IPR00777; GP120.
Indels	0;	Gaps	0;		DR	pFan: PF00516; GP120; 1.
OQ	3 ETLMDQDQRQLNSWGWGCAFQVCHTTVPM 634	Db	608 EKYLQDQARLNNSWGWGCAFQVCHTTVPM 634		DR	AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;

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CC		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
DR	InterPro; IPR000777; GP120.	CC	
DR	Pfam; PF00516; GP120; 1.	CC	
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal..	CC	
FT	SIGNAL 1 : 24	CC	
FT	CHAIN 25 : 522	CC	
FT	CHAIN 523 : 854	CC	
FT	CARBOHYD 35 : 35	CC	
FT	CARBOHYD 68 : 68	CC	
FT	CARBOHYD 115 : 115	CC	
FT	CARBOHYD 136 : 136	CC	
FT	CARBOHYD 153 : 153	CC	
FT	CARBOHYD 168 : 168	CC	
FT	CARBOHYD 182 : 182	CC	
FT	CARBOHYD 199 : 199	CC	
FT	CARBOHYD 244 : 244	CC	
FT	CARBOHYD 255 : 255	CC	
FT	CARBOHYD 265 : 265	CC	
FT	CARBOHYD 271 : 271	CC	
FT	CARBOHYD 283 : 283	CC	
FT	CARBOHYD 295 : 295	CC	
FT	CARBOHYD 305 : 305	CC	
FT	CARBOHYD 355 : 355	CC	
FT	CARBOHYD 400 : 400	CC	
FT	CARBOHYD 409 : 409	CC	
FT	CARBOHYD 458 : 458	CC	
FT	CARBOHYD 472 : 472	CC	
FT	CARBOHYD 478 : 478	CC	
FT	CARBOHYD 623 : 623	CC	
FT	CARBOHYD 624 : 624	CC	
FT	CARBOHYD 630 : 630	CC	
FT	CARBOHYD 646 : 646	CC	
SO	SEQUENCE 854 AA: 98855 MW: 5919CAC6GC9622912F CRC64: 620	CC	
Query Match 50.3%; Score 87; DB 1; Length 854;	Best Local Similarity 48.1%; Pred. No. 2.2e-05;	RL	Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).
Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;		CC	
QY 3 ETLMQDOQRNLNSWGCKGKIIICVTSARW 29	QY 3 ETLMQDOQRNLNSWGCKGKIIICVTSARW 29	CC	
594 EKYIKDQAQLNSWGCAFRQVCHTSVPW 620	594 EKYIKDQAQLNSWGCAFRQVCHTSVPW 600	CC	
RESULT 6	Query Match 50.3%; Score 87; DB 1; Length 856;	CC	
TD ENV_HV2NZ STANDARD; PRT: 856 AA.	Best Local Similarity 51.9%; Pred. No. 2.2e-05;	CC	
TD ENV_HV2NZ STANDARD; PRT: 856 AA.	Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;	CC	
AC P05883; 01-NOV-1988 (Rel. 09, Created)		CC	
DT 01-NOV-1988 (Rel. 09, Last sequence update)		CC	
DT 15-JUL-1999 (Rel. 38, Last annotation update)		CC	
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		CC	
DE Glycoprotein (GP120); Transmembrane glycoprotein (GP41). [1]		CC	
DE Sequence from N.A. ENV.		CC	
OS Human immunodeficiency virus type 2 (isolate NIH-Z) (HIV-2).		CC	
OC Viruses; Retroviridae; Lentivirus.		CC	
OX NCBI_TaxID=11719;		CC	
RN [1]		CC	
RP Sequence from N.A. ENV.		CC	
RX MEDLINE-88320359; PubMed=3261862;		CC	
RA Zagury J.F., Franchini G., Reitz M.S. Jr., Collalati E., Starcich B.R., Hall L., Fargnoli K., Jagodzinski L.L., Guo H.-G., Laure F., Arya S.K., Josephs S.P., Zagury D., Wong-Staal F., Gallo R.C.;		CC	
RT "Genetic variability between isolates of human immunodeficiency virus (HIV) type 2 is comparable to the variability among HIV type 1";		CC	
RT		CC	
RESULT 7	Query Match 50.3%; Score 87; DB 1; Length 856;	CC	
TD ENV_HV2SB STANDARD; PRT: 846 AA.	Best Local Similarity 51.9%; Pred. No. 2.2e-05;	CC	
TD ENV_HV2SB STANDARD; PRT: 846 AA.	Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;	CC	
AC P12449; 01-OCT-1989 (Rel. 12, Created)		CC	
DT 01-OCT-1989 (Rel. 12, Last sequence update)		CC	
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		CC	
DE Glycoprotein (GP120); Transmembrane glycoprotein (GP41). [1]		CC	
DE Human immunodeficiency virus type 2 (isolate SBL1SY) (HIV-2).		CC	
OC Viruses; Retroviridae; Lentivirus.		CC	
OX NCBI_TaxID=11718;		CC	





FT	DISULFID	125	194	BY SIMILARITY.	CC	modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> ) or send an email to license@isb-sib.ch).
FT	DISULFID	130	155	BY SIMILARITY.	CC	
FT	DISULFID	216	245	BY SIMILARITY.	CC	
FT	DISULFID	226	237	BY SIMILARITY.	CC	
FT	DISULFID	294	328	BY SIMILARITY.	CC	
FT	DISULFID	374	435	BY SIMILARITY.	CC	
FT	DISULFID	381	408	BY SIMILARITY.	DR	InterPro; IPR00328; Env_SP41.
FT	CARBONYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	InterPro; IPR00777; GP20.
FT	CARBONYD	135	135	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	Pfam; PF00516; GP120; 1.
FT	CARBONYD	154	154	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	Pfam; PF00517; GP1; 1.
FT	CARBONYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL).	AIDS	HIV; M12507; AAB12990.1; -.
FT	CARBONYD	195	195	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	HIV; M12507; ENV_SWWJ2.
FT	CARBONYD	232	232	N-LINKED (GLCNAC. . .) (POTENTIAL).	SIGNAL	1. 29
FT	CARBONYD	239	239	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CHAIN 30 501
FT	CARBONYD	260	260	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CHAIN 502 847
FT	CARBONYD	274	274	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	DISULFID 53 73
FT	CARBONYD	293	293	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	DISULFID 118 202
FT	CARBONYD	299	299	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	DISULFID 125 193
FT	CARBONYD	329	329	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	DISULFID 130 152
FT	CARBONYD	336	336	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	DISULFID 215 244
FT	CARBONYD	352	352	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	DISULFID 225 236
FT	CARBONYD	382	382	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	DISULFID 293 326
FT	CARBONYD	388	388	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	DISULFID 372 435
FT	CARBONYD	392	392	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	DISULFID 379 408
FT	CARBONYD	398	398	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBONYD 87 87
FT	CARBONYD	401	401	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBONYD 134 134
FT	CARBONYD	438	438	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBONYD 140 140
FT	CARBONYD	454	454	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBONYD 151 151
FT	CARBONYD	602	602	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBONYD 155 155
FT	CARBONYD	607	607	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBONYD 183 183
FT	CARBONYD	616	616	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBONYD 184 184
FT	CARBONYD	628	628	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBONYD 194 194
SO	SEQUENCE	847 AA;	96135 MW;	0A901317FD7F2AB CRC64;		
Query Match	49.1%	Score 85; DB 1; Length 847;				
Best Local Similarity	46.4%	Pred. No. 4.4e-05;				
Matches	13;	Conservative	6;	Mismatches	9;	Indels 0; Gaps 0;
OY	3	ETLMQDQQLNSWCKGRICIVSARWH 30				
Db	575	ERYLRDQQQLINGCSGKLICITTPVWN 602				
RESULT 11						
ENV_HV1W2						
ID	ENV_HV1W2	STANDARD;	PRT;	847 AA.		
AC	P05880;					
PT	01-NOV-1988 (Rel. 09, Created)					
PT	01-NOV-1988 (Rel. 09, Last sequence update)					
PT	15-JUL-1999 (Rel. 38, Last annotation update)					
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].					
GN	ENV.					
OS	Human immunodeficiency virus type 1 (HIV2 isolate) (HIV-1).					
OC	Viruses; Retroviridae; Lentivirus.					
OX	NCBL_TaxId:11705;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE:86235450, PubMed=3012778;					
RA	Hahn B.H., Show G.N., Taylor M.E., Reiffeld R.R., Markham P.D.,					
RA	Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks W.P.;					
RT	"Genetic variation in HIV-1/LAV over time in patients with AIDS or at risk for AIDS,"					
RT	Science 232:1548-1553(1986).					
RL	-- MISCCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERTINENTLY INFECTED BY HER MOTHER.					
CC						
CC						
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Query Match	49.1%	Score 85; DB 1; Length 847;				
Best Local Similarity	46.4%	Pred. No. 4.4e-05;	6;	Mismatches	9;	Indels 0; Gaps 0;
OY	3	ETLMQDQQLNSWCKGRICIVSARWH 30				
Db	575	ERYLRDQQQLINGCSGKLICITTPVWN 602				
RESULT 12						
ENV_HV1B8						
ID	ENV_HV1B8	STANDARD;	PRT;	851 AA.		
AC	P05882;					
PT	13-AUG-1987 (Rel. 05, Created)					
PT	13-AUG-1987 (Rel. 05, Last sequence update)					
PT	15-JUL-1999 (Rel. 38, Last annotation update)					
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].					



FT CARBOHYD 234 234 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 241 241 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 262 262 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 276 276 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 289 289 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 295 295 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 301 301 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 331 331 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 354 354 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 360 360 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 384 384 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 390 390 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 396 396 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 400 400 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 456 456 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 607 607 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 612 612 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 621 621 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 633 633 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 670 670 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 812 812 SEQUENCE 852 AA; 97203 MW; 2BB866345DEC915F CRC64;

Query Match  
 Best Local Similarity 49.1%; Score 85; DB 1; Length 852;  
 Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 3 ETLMDQDQRQLNSWGCGRICITYSARWH 30  
 Db 580 ERYLRDQQQLGIWGCGSKLICTTAVPWN 607

RESULT 14  
 ENV\_HV1S3 STANDARD; PRT: 852 AA.

AC P19549; DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.  
 OS Human immunodeficiency virus type 1 (SF3 isolate) (HIV-1).  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11690;  
 RN [1]

RP SEQUENCE FROM N.A.  
 MEDLINE=90317906; PubMed=2370688;  
 RA York Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;  
 RT "Human immunodeficiency virus type 1 cellular host range,  
 replication, and cytopathicity are linked to the envelope region of  
 the viral genome." J. Virol. 64:4016-4020(1990).

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CC EMBL: M38427; AAA45067.1; - .

DR InterPro; IPR000328; Env-GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 206 BY SIMILARITY.  
 FT DISULFID 125 197 BY SIMILARITY.  
 FT DISULFID 130 156 BY SIMILARITY.  
 FT DISULFID 219 248 BY SIMILARITY.  
 FT DISULFID 229 240 BY SIMILARITY.  
 FT DISULFID 297 331 BY SIMILARITY.  
 FT DISULFID 377 439 BY SIMILARITY.  
 FT DISULFID 384 412 BY SIMILARITY.  
 FT CARBOHYD 87 87 BY SIMILARITY.  
 FT CARBOHYD 129 129 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 136 136 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 141 141 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 142 142 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 155 155 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 159 159 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 189 189 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 198 198 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 263 263 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 277 277 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 290 290 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 296 296 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 332 332 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 339 339 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 355 355 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 385 385 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 391 391 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 397 397 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 401 401 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 405 405 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 457 457 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 607 607 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 612 612 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 621 621 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 633 633 N-LINKED 'GLCNAC. . ) (POTENTIAL).  
 FT CARBOHYD 812 812 SEQUENCE 852 AA; 96663 MW; EE7BBF8D3C9910D CRC64;

Query Match  
 Best Local Similarity 49.1%; Score 85; DB 1; Length 852;  
 Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 3 ETLMDQDQRQLNSWGCGRICITYSARWH 30  
 Db 580 ERYLRDQQQLGIWGCGSKLICTTAVPWN 607

RESULT 15  
 ENV\_HV1MF STANDARD; PRT: 853 AA.

AC P19551; DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)

DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

ENV Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).  
 OS Viruses; Retroviridae; Lentivirus.  
 OC NCBI\_TaxID=11704;

RN RP SEQUENCE FROM N.A.  
 MEDLINE=90317906; PubMed=1695254;  
 RA Stevenson M., Haggerty S., Lamontica C., Mann A.M., Meier C., Wasik A.; Cloning and characterization of human immunodeficiency virus type 1 variants diminished in the ability to induce syncytium-independent cytolysis.";

FT SIGNAL 1 31 BY SIMILARITY.

**Query Match** 49.1%; **Score** 85; **DB** 1; **Length** 853;  
**Best Local Similarity** 46.4%;  
**Pred. No.** 4.5e-05; **Matches** 6; **Mismatches** 9; **Indels** 0; **Gaps** 0;

QY 3 ETLMQDQQLNNSWCKGRICYTSARWH 30  
   | ::::| - ||-| :|| | :| :|  
 Db 582 ERYLKDQQLGIWGCGSKLICITTAWPWN 609



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KW Transmembrane.  
 FT 1  
 NON\_TER 1  
 SEQUENCE 143 AA; 16331 MW; 15A17063CCD3431D CRC64;

Query Match 74.0%; Score 128; DB 15; Length 143;  
 Best Local Similarity 75.0%; Pred. No. 3.9e-12; DR KW  
 Matches 21; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY |||:|||:|||||:|||||:|||:  
 Db 61 ETLMONQQLNLWGCKGRIVCYTSVRWN 88

RESULT 14

ID Q79670 PRELIMINARY; PRT: 876 AA.  
 AC 079670: 01-NOV-1996 (TREMBREL. 01, Created)  
 DT 01-NOV-1996 (TREMBREL. 01, Last sequence update)  
 RT 01-NOV-1996 (TREMBREL. 19, Last annotation update)

DE ENVELOPE PROTEIN GP120/GP41.  
 GN ENV.

OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Lentivirus.  
 OX NCBI\_TAXID=11676;  
 RN [1]

SEQUENCE FROM N.A.

RX Gurtler L.G., Hauser P.H., Eberle J., von Brunn A., Knap S.,  
 RA Zekeng L., Tsague J.M., Kaptev L.;  
 RT "A new subtype of human immunodeficiency virus type 1 (MWP-5180) from  
 Cameroon." J Virol. 68:1561-1564 (1994).  
 DR EMBL; L20571; AA:A44064.1;  
 DR InterPro; IPR000328; Env GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 KW SEQUENCE 876 AA; 99245 MW; A92F88E37522BAB CRC64;

Query Match 74.0%; Score 128; DB 15; Length 876;  
 Best Local Similarity 71.4%; Pred. No. 2.8e-11; DR KW  
 Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 ETLMQDQRNLNSGCKGRIVCYTSVRWN 30  
 Db 596 ETLMONQQLNLWGCKGRIVCYTSVRWN 623

RESULT 15

ID O11939 PRELIMINARY; PRT: 105 AA.  
 AC 011939; 01-JUL-1997 (TREMBREL. 04, Created)  
 DT 01-JUL-1997 (TREMBREL. 04, Last sequence update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN ENV.

OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Lentivirus.  
 OX NCBI\_TAXID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN\_AB7063;  
 RX MEDLINE=97340011; PubMed=9197385;  
 RA Breman C.A., Hackett J., Zekeng L., Lund J.K., Vallari A.S.,  
 RA Hickman R.K., Gurtler L., Kaptev L., von Overbeck J., Hampl H.,  
 Devre S.G.;  
 RT \*Sequence of gp41env immunodominant region of HIV type 1 group O from

RT west central Africa;"  
 RL AIDS Res. Hum. Retroviruses 13:901-904 (1997).  
 DR EMBL; U90132; AAB62815.1; -  
 DR InterPro; IPR000328; Env GP41.  
 DR Pfam; PF00517; GP41; 1.  
 FT NON\_TER 1  
 KW Transmembrane.  
 DR KW  
 FT NON\_TER 1  
 SQ SEQUENCE 105 AA; 12531 MW; 2D3D6B5BADC4A382 CRC64;

Query Match 73.4%; Score 127; DB 15; Length 105;  
 Best Local Similarity 71.4%; Pred. No. 4e-12; DR KW  
 Matches 20; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 ETLMQDQRNLNSGCKGRIVCYTSVRWN 30  
 Db 24 ETLMONQQLNLWGCKGRIVCYTSVRWN 51

Search completed: August 15, 2002, 10:49:45  
 Job time: 199 sec

Thu Aug 15 11:07:55 2002

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